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SEQUENCE LISTING

<110> Degussa AG

5 <120> Mutants for the preparation of D-amino acids

<130> 020453 AM

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<170> PatentIn Ver. 2.1

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<211> 948

<212> DNA

<213> Arthrobacter crystallopoietes

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Glu Glu Ala Ala Ser Gln Gly Ala Glu Leu Val Val Phe Pro Glu Leu	
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40 acg ctg acc acg ttc ttc ccg cgt acc tgg ttc gaa gaa ggc gac ttc	192
Thr Leu Thr Thr Phe Phe Pro Arg Thr Trp Phe Glu Glu Gly Asp Phe	
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45 gag gaa tac ttc gat aaa tcc atg ccc aat gac gac gtc gcg ccc ctt	240
Glu Glu Tyr Phe Asp Lys Ser Met Pro Asn Asp Asp Val Ala Pro Leu	
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50 ttc gaa cgc gcc aaa gac ctt ggc gtg ggc ttc tac ctc gga tac gcg	288
Phe Glu Arg Ala Lys Asp Leu Gly Val Gly Phe Tyr Leu Gly Tyr Ala	
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55 gaa ctg acc agt gat gag aag cgg tac aac aca tca att ctg gtg aac	336
Glu Leu Thr Ser Asp Glu Lys Arg Tyr Asn Thr Ser Ile Leu Val Asn	
100 105 110	

55 aag cac ggc gac atc gtc ggc aag tac cgc aag atg cat ctg ccg ggc	384
Lys His Gly Asp Ile Val Gly Lys Tyr Arg Lys Met His Leu Pro Gly	
115 120 125	

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His Ala Asp Asn Arg Glu Gly Leu Pro Asn Gln His Leu Glu Lys Lys	

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15	tac cgc tct ttg gcc ctg cag gga gca gag ctc gtc gtc ctg ggc tac Tyr Arg Ser Leu Ala Leu Gln Gly Ala Glu Leu Val Val Leu Gly Tyr 180 185 190			576
20	aac acc ccc gat ttc gtt ccc ggc tgg cag gaa gag cct cac gcg aag Asn Thr Pro Asp Phe Val Pro Gly Trp Gln Glu Glu Pro His Ala Lys 195 200 205			624
25	atg ttc acg cac ctt ctt tca ctt cag gca ggg gca tac cag aac tcg Met Phe Thr His Leu Leu Ser Leu Gln Ala Gly Ala Tyr Gln Asn Ser 210 215 220			672
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 5 Thr Leu Thr Thr Phe Phe Pro Arg Thr Trp Phe Glu Glu Gly Asp Phe
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 Glu Glu Tyr Phe Asp Lys Ser Met Pro Asn Asp Asp Val Ala Pro Leu
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 10 Phe Glu Arg Ala Lys Asp Leu Gly Val Gly Phe Tyr Leu Gly Tyr Ala
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 100 105 110
 15 Lys His Gly Asp Ile Val Gly Lys Tyr Arg Lys Met His Leu Pro Gly
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 130 135 140
 Tyr Phe Arg Glu Gly Asp Leu Gly Phe Gly Val Phe Asp Phe His Gly
 145 150 155 160
 25 Val Gln Val Gly Met Cys Leu Cys Asn Asp Arg Arg Trp Pro Glu Val
 165 170 175
 Tyr Arg Ser Leu Ala Leu Gln Gly Ala Glu Leu Val Val Leu Gly Tyr
 180 185 190
 30 Asn Thr Pro Asp Phe Val Pro Gly Trp Gln Glu Glu Pro His Ala Lys
 195 200 205
 Met Phe Thr His Leu Leu Ser Leu Gln Ala Gly Ala Tyr Gln Asn Ser
 210 215 220
 Val Phe Val Ala Ala Ala Gly Lys Ser Gly Phe Glu Asp Gly His His
 225 230 235 240
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 245 250 255
 Lys Ala Ala Gly Glu Gly Asp Glu Val Val Val Val Lys Ala Asp Ile
 260 265 270
 45 Asp Met Gly Lys Pro Tyr Lys Glu Ser Val Phe Asp Phe Ala Ala His
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<213> *Arthrobacter crystallopoietes*

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Lys Ile Arg Ala Asp Val Leu Ile Glu Asn Gly Lys Val Ala Ala Val
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Gly Met Leu Asp Ala Ala Thr Pro Asp Thr Val Glu Arg Val Asp Cys
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Asp Gly Lys Tyr Val Met Pro Gly Gly Ile Asp Val His Thr His Ile
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Asp Ser Pro Leu Met Gly Thr Thr Thr Ala Asp Asp Phe Val Ser Gly
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Thr Ile Ala Ala Ala Thr Gly Gly Thr Thr Thr Ile Val Asp Phe Gly
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Gln Gln Leu Ala Gly Lys Asn Leu Leu Glu Ser Ala Asp Ala His His
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Lys Lys Ala Gln Gly Lys Ser Val Ile Asp Tyr Gly Phe His Met Cys
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Val Thr Asn Leu Tyr Asp Asn Phe Asp Ser His Met Ala Glu Leu Thr
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Gln Asp Gly Ile Ser Ser Phe Lys Val Phe Met Ala Tyr Arg Gly Ser
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165 170 175
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Asp Arg Ile Ala Ala Asp Leu Tyr Ala Gln Gly Lys Thr Gly Pro Gly
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40	atc	ccc	aac	ggc	ggg	ccc	ggc	gtg	gag	cac	cga	atg	ctc	gtg	atg	tat	1056
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25 Asp Gly Lys Tyr Val Met Pro Gly Gly Ile Asp Val His Thr His Ile
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30 Thr Ile Ala Ala Ala Thr Gly Gly Thr Thr Thr Ile Val Asp Phe Gly
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45 Leu Met Ile Asn Asp Gly Glu Leu Phe Asp Ile Leu Lys Gly Val Gly
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50 Asp Arg Ile Ala Ala Asp Leu Tyr Ala Gln Gly Lys Thr Gly Pro Gly
    195              200              205

55 Thr His Glu Ile Ala Arg Pro Pro Glu Ser Glu Val Glu Ala Val Ser
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 Ser Arg Asp Ile Tyr Asp Gln Pro Gly Phe Glu Pro Ala Lys Ala Val
 275 280 285
 10 Leu Thr Pro Pro Leu Arg Thr Gln Glu His Gln Asp Ala Leu Trp Arg
 290 295 300
 15 Gly Ile Asn Thr Gly Ala Leu Ser Val Val Ser Ser Asp His Cys Pro
 305 310 315 320
 Phe Cys Phe Glu Glu Lys Gln Arg Met Gly Ala Asp Asp Phe Arg Gln
 325 330 335
 20 Ile Pro Asn Gly Gly Pro Gly Val Glu His Arg Met Leu Val Met Tyr
 340 345 350
 Glu Thr Gly Val Ala Glu Gly Lys Met Thr Ile Glu Lys Phe Val Glu
 355 360 365
 25 Val Thr Ala Glu Asn Pro Ala Lys Gln Phe Asp Met Tyr Pro Lys Lys
 370 375 380
 30 Gly Thr Ile Ala Pro Gly Ser Asp Ala Asp Ile Ile Val Val Asp Pro
 385 390 395 400
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 405 410 415
 35 Tyr Thr Leu Phe Glu Gly Phe Lys Ile Arg Cys Ser Ile Asp Gln Val
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 Phe Ser Arg Gly Asp Leu Ile Ser Val Lys Gly Glu Tyr Val Gly Thr
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